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5'	9	18	27	36	45	54											
ATG	GCC	ATC	ACC	CAG	TTT	CGG	TTA	TTT	AAA	TTT	TGT	ACC	TGC	CTA	GCA	ACA	GTA
M	A	I	T	Q	F	R	L	F	K	F	C	T	C	L	A	T	V
TM																	
63	72	81	90	99	108												
TTC	TCA	TTC	CTA	AAG	AGA	TTA	ATA	TGC	AGA	TCT	GGC	AGA	GGA	CGG	AAA	TTA	AGT
F	S	F	L	K	R	L	I	C	R	S	G	R	G	R	K	L	S
117	126	135	144	153	162												
GGA	GAC	CAA	ATA	ACT	TIG	CCA	ACT	ACA	GTT	GAT	TAT	TCA	TCA	GTT	CCT	AAG	CAG
G	D	Q	I	T	L	P	T	T	V	D	Y	S	S	V	P	K	Q
171	180	189	198	207	216												
ACA	GAT	GTT	GAA	GAG	TGG	ACT	TCC	TGG	GAT	GAA	GAT	GCA	CCC	ACC	AGT	GTA	AAG
T	D	V	E	E	W	T	S	W	D	E	D	A	P	T	S	V	K

FIG. 1A

225	234	243	252	261	270
ATC GAA GGA GGG AAT GGG AAT GTG GCA ACA CAA AAT TCT TTG GAA CAA CTG					
I E G G N G N V A T Q Q N S L E Q L					
279	288	297	306	315	324
GAA CCT GAC TAT TTT AAG GAC ATG ACA CCA ACT ATT AGG AAA ACT CAG AAA ATT					
E P D Y F K D M T P T I R K Q K I					
333	342	351	360	369	378
GTT ATT AAG AAG AGA GAA CCA TTG AAT TTT GGC ATC CCA GAT GGG AGC ACA GGT					
V I K K R E P L N F G I P D G S T G					
387	396	405	414	423	432
TTC TCT AGT AGA TTA GCA GCT ACA CAA GAT CTG CCT TTT ATT CAT CAG TCT TCT					
F S S R L A A T Q D L P F I H Q S S					

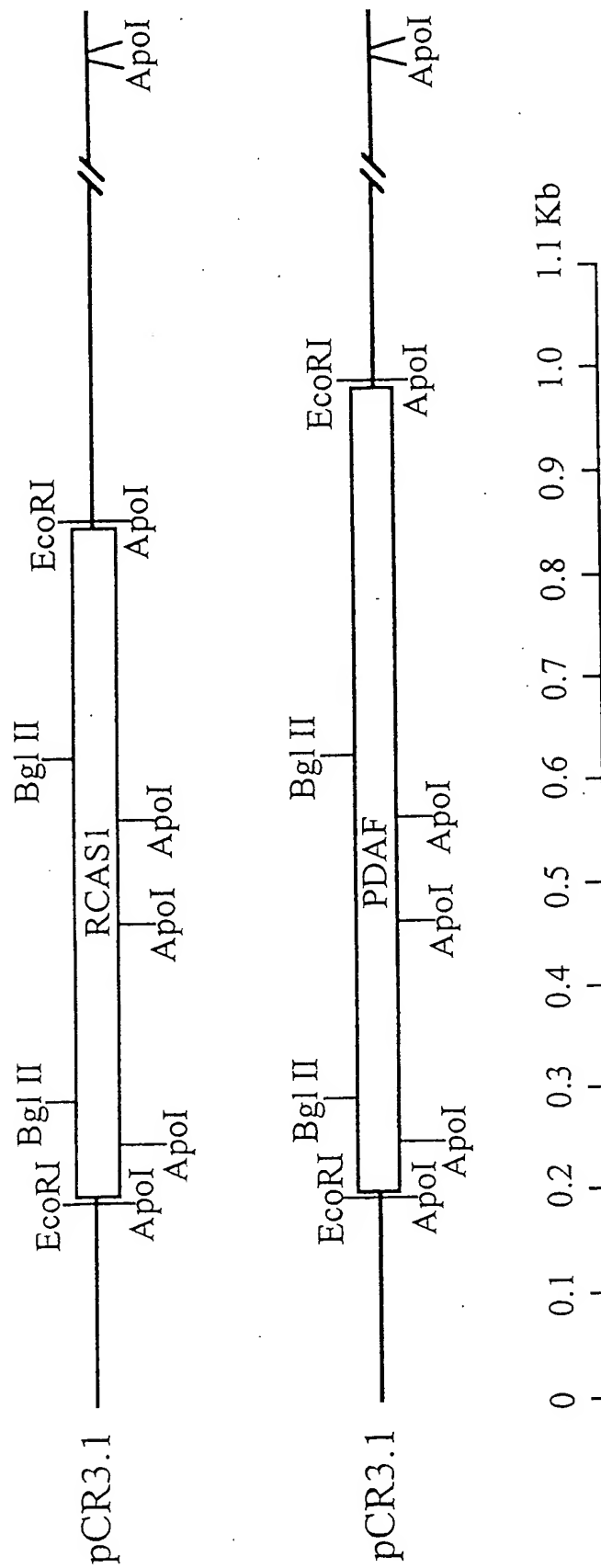
FIG. 1B

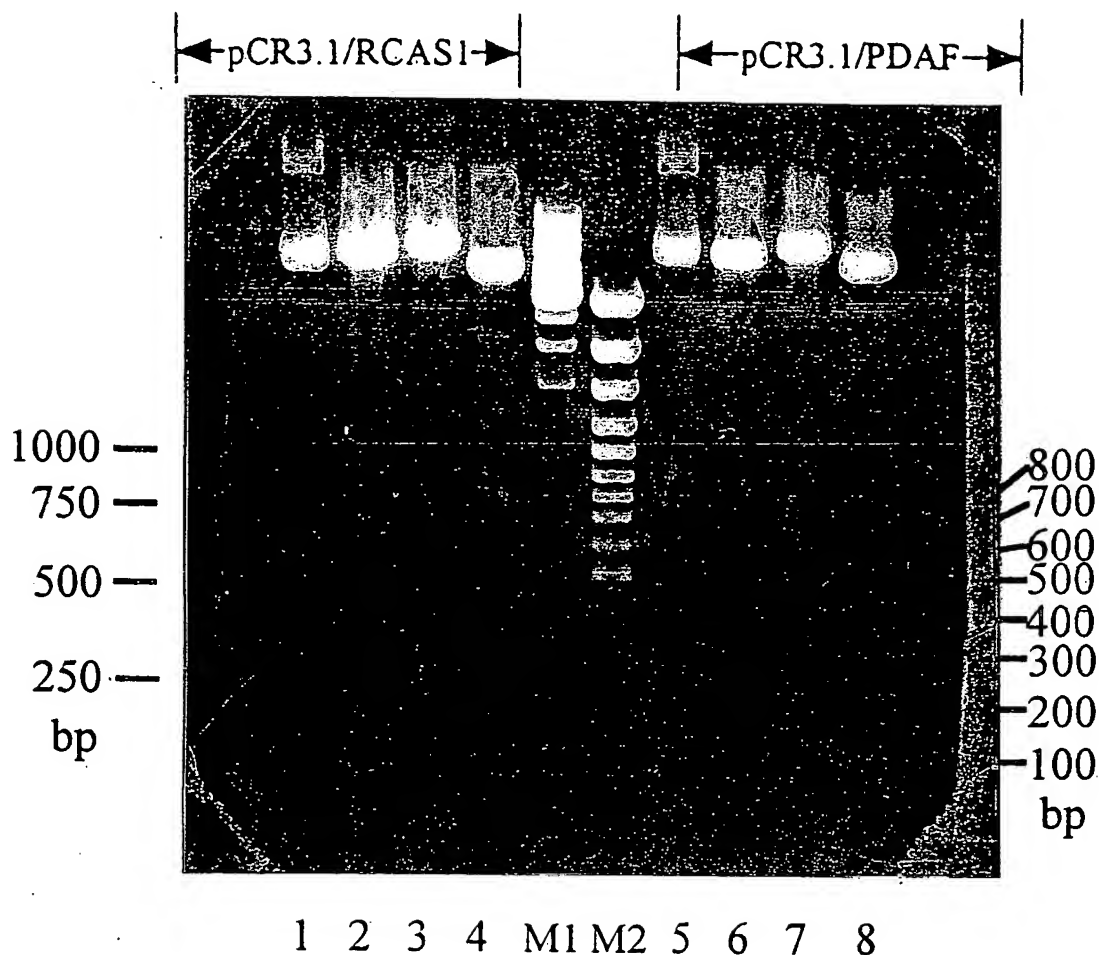
441	450	459	468	477	486
GAA TTA GGT GAC TTA GAT ACC TGG CAG GAA AAT ACC AAT GCA TGG GAA GAA GAA					
---	---	---	---	---	---
E L G D L D T W Q E N T N A W E E E					
---	---	---	---	---	---
495	504	513	522	531	540
GAA GAT GCA GCC TGG CAA GCA GAA GAT GTT CTG AGA TCC AGG ACC AAT GTA TGT					
---	---	---	---	---	---
E D A A W Q A E E V L R					
---	---	---	---	---	---
				S R T N V C	
549	558	567	576	585	594
TTA CTC TGC TCT CTC CIG TTT CAT CAT CCC ACT CCT ACC TCC ACT CCC TAC ATT					
---	---	---	---	---	---
L L C S L L F H H P T P T S T P Y I					
---	---	---	---	---	---
603	612	621	630	639	648
AAC CAA TCA GTA AAG ATA GAG AGA GTG AGT CTG GGT CAG TGG AGT TAC GGA AAG					
---	---	---	---	---	---
N Q S V K I E R V S L					
---	---	---	---	---	---
			G Q W S Y G K		

FIG. 1C

Box region: a novel peptide consists of 45 amino acids in the PDAF protein
Shadow region: ATP-GTP binding site motif
Underline region: TM - transmembrane domain
DIM - coiled coil structure and dimeric domain

FIG. 1D.





lane1 & 5: uncut

lane2 & 6: EcoRI cut

lane3 & 7: Bgl II cut

lane4 & 8: Apo I cut

M1:GeneRuler™ 1Kb DNA Ladder

M2:GeneRuler™ 100bp DNA Ladder Plus

FIG. 2B

PDAF 185 LLFHHPTPTSTPYINQSVKIERVSLGQWS 213
L+ HH P ++ S+ I+R+ GQW+

PIG-B 256 LILLHHFLPVGFVTLSSLMLIDRIFFGQWT 284

Identities = 10/29 (34%)
Positives = 17/29 (58%)

FIG. 3

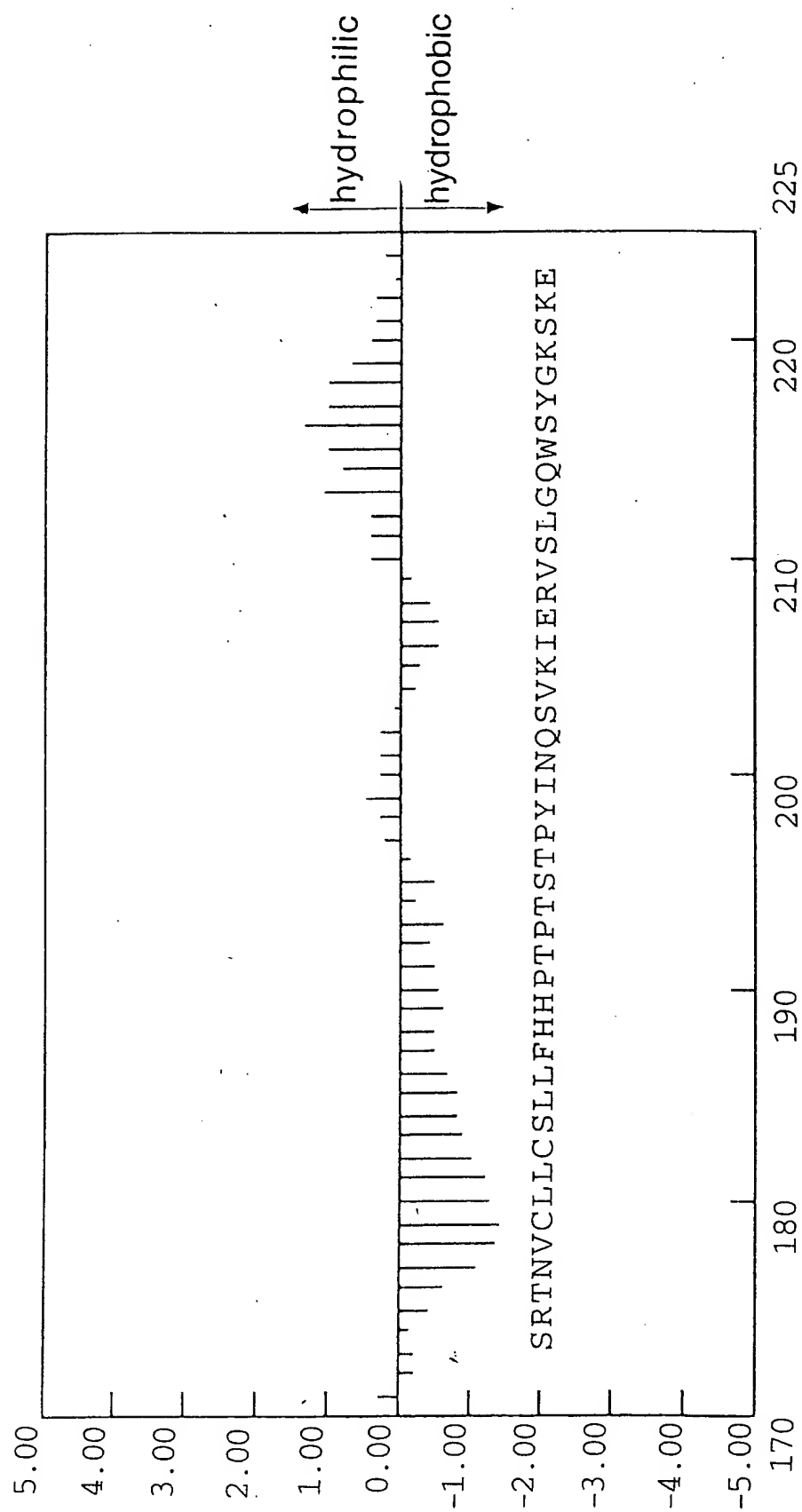
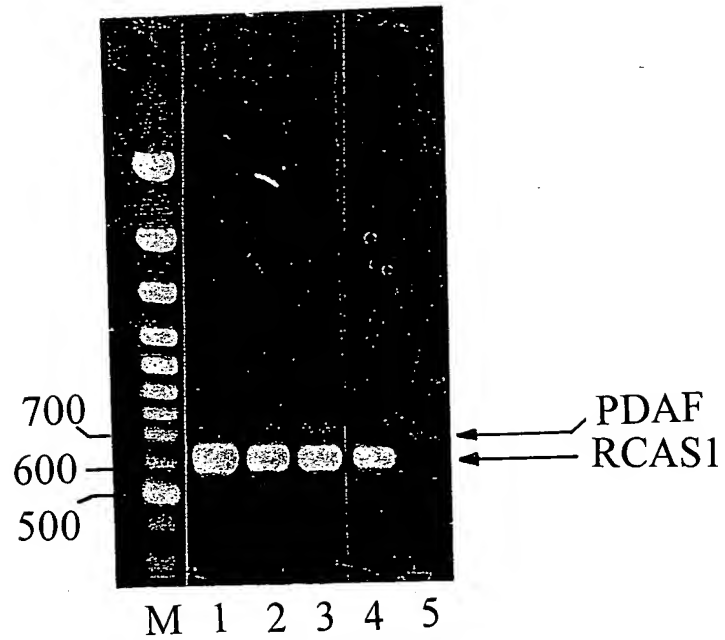


FIG. 4



M: 100 bp DNA marker
lane1: MCF7
lane2: HT29
lane3: RD
lane4: A375
lane5: placenta

FIG. 5

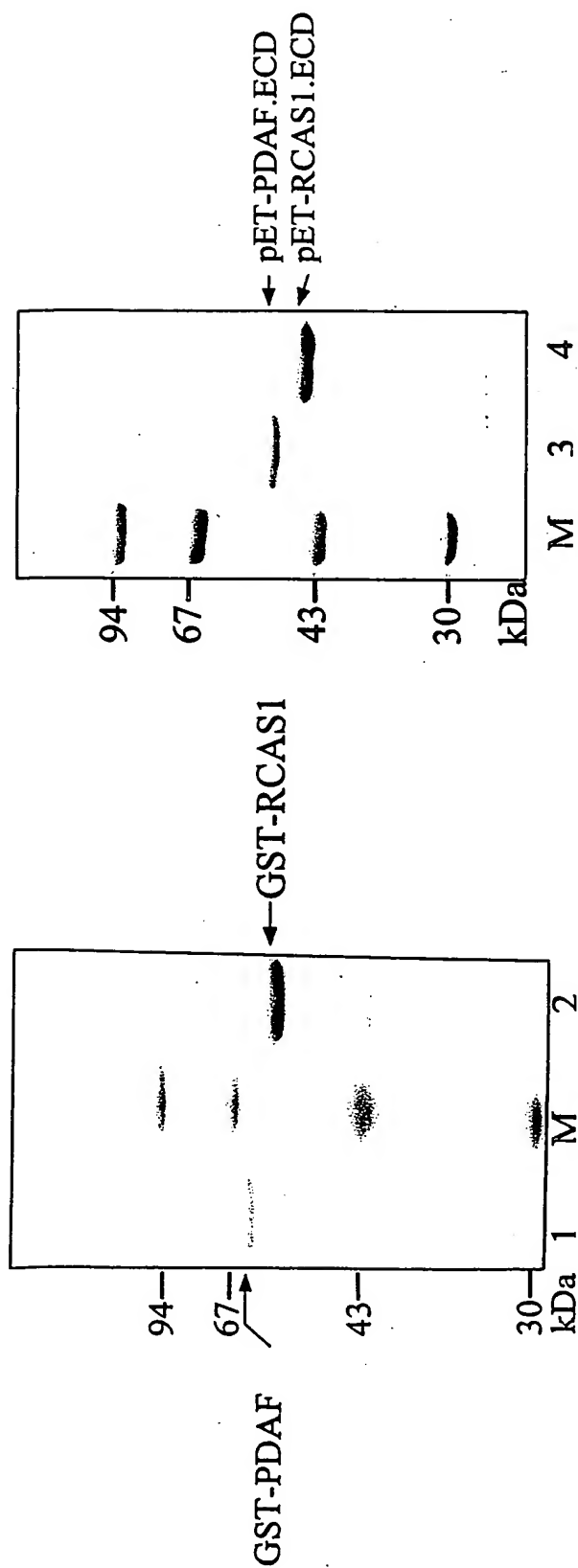
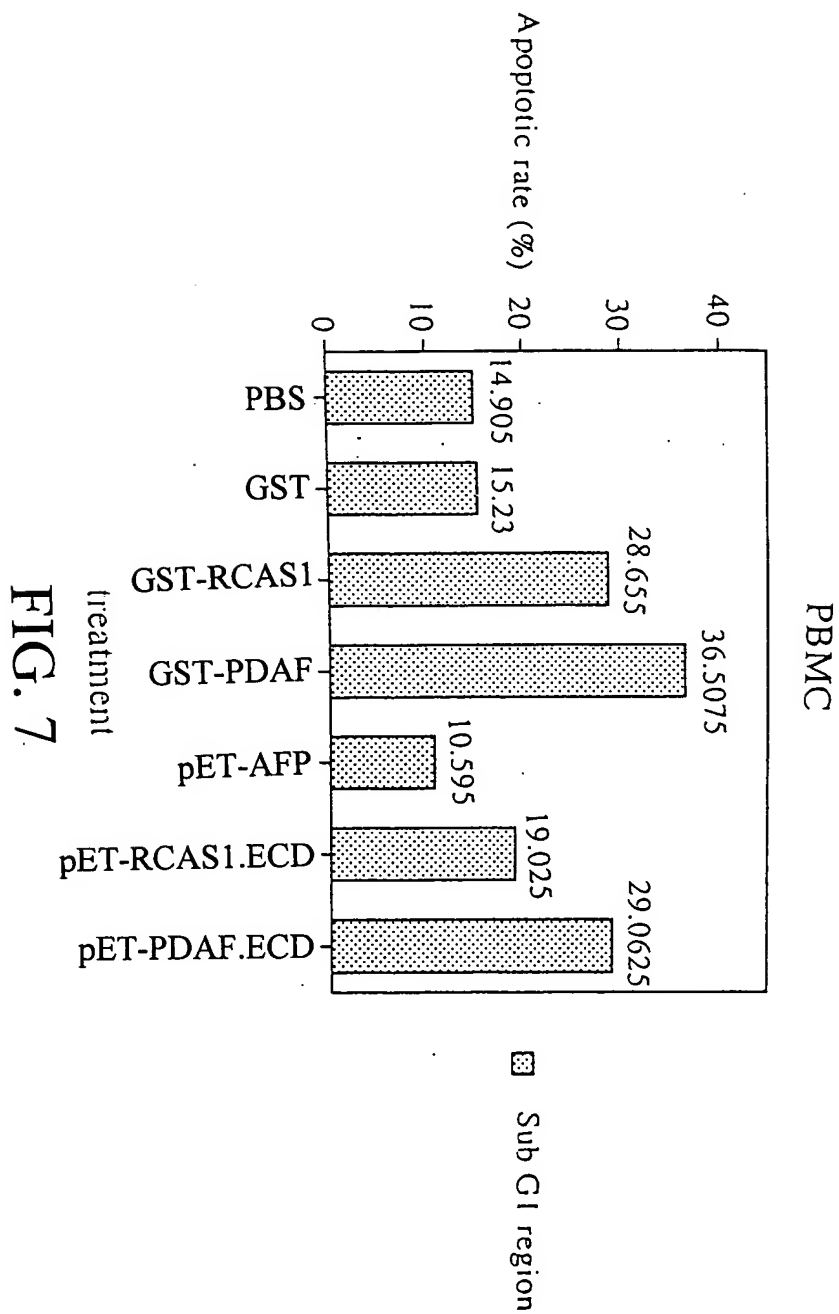


FIG. 6



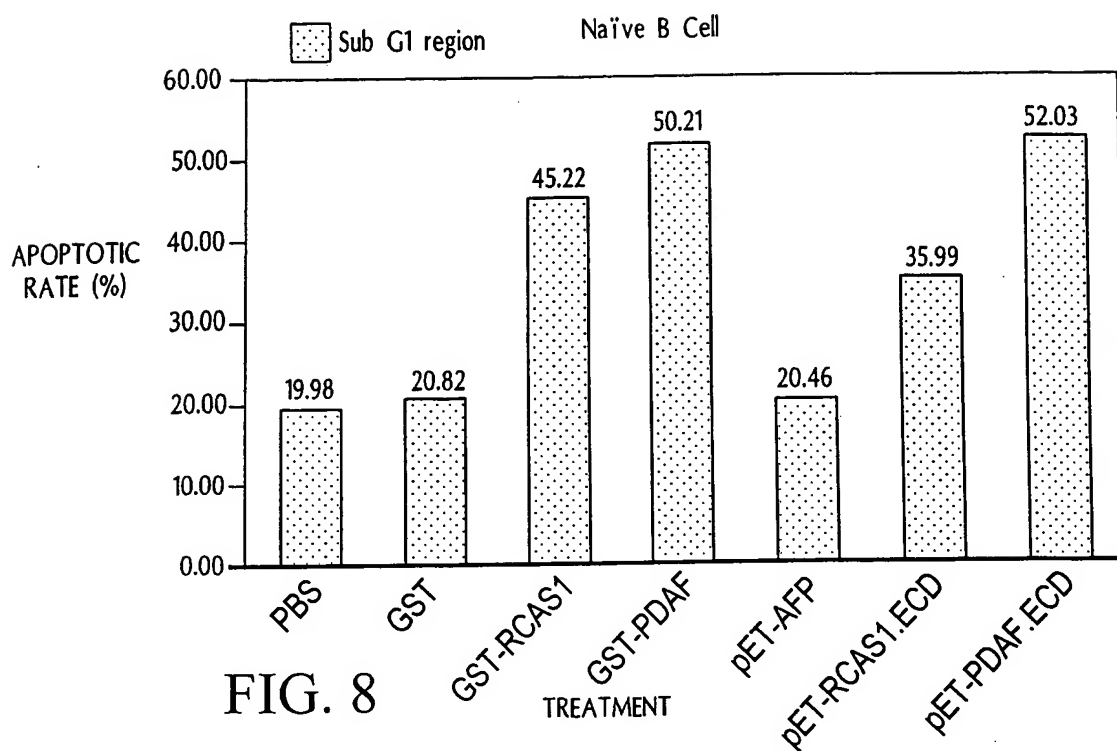


FIG. 8

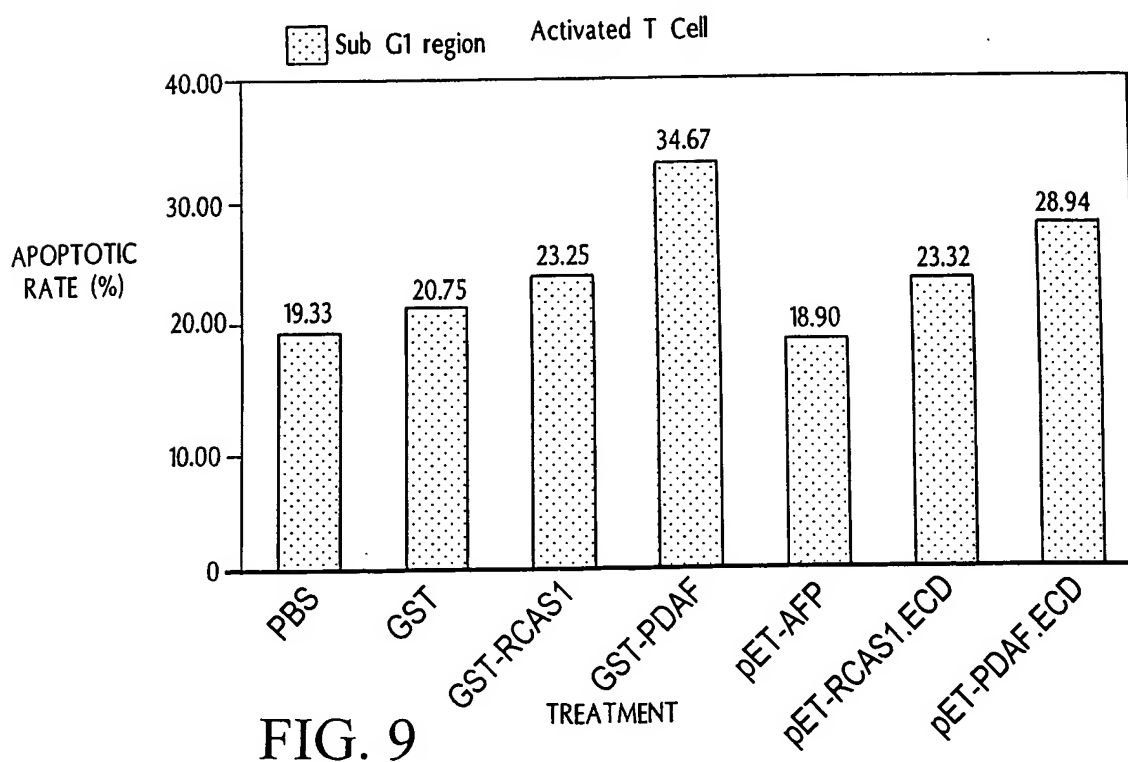


FIG. 9

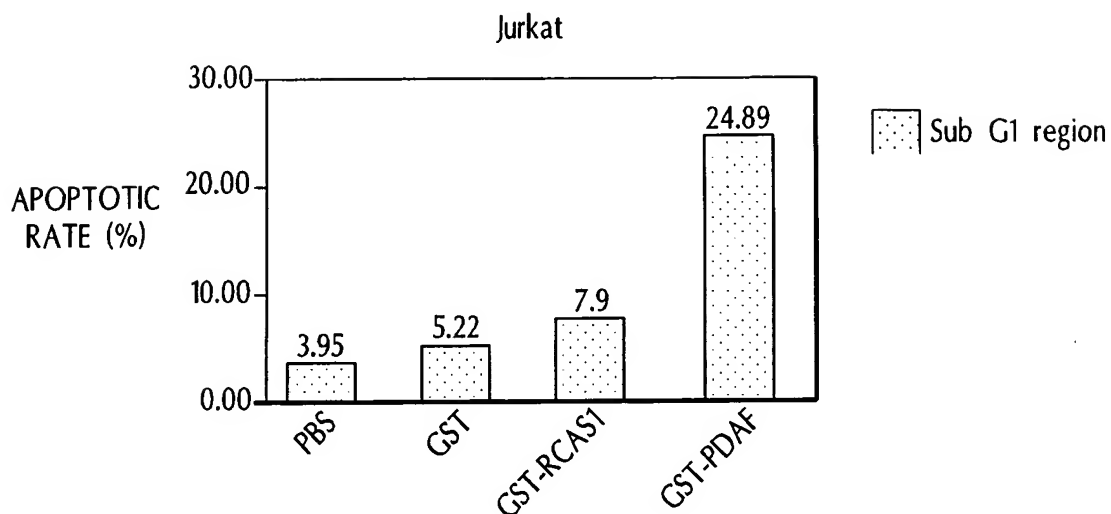


FIG. 10

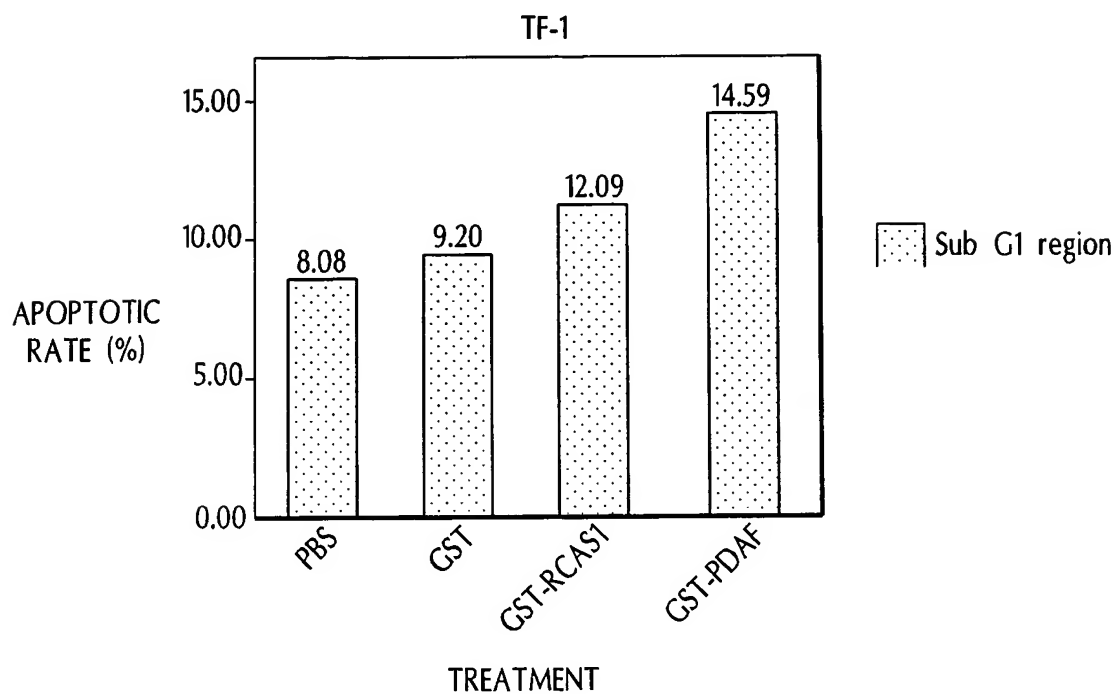


FIG. 11